FIGURE 1

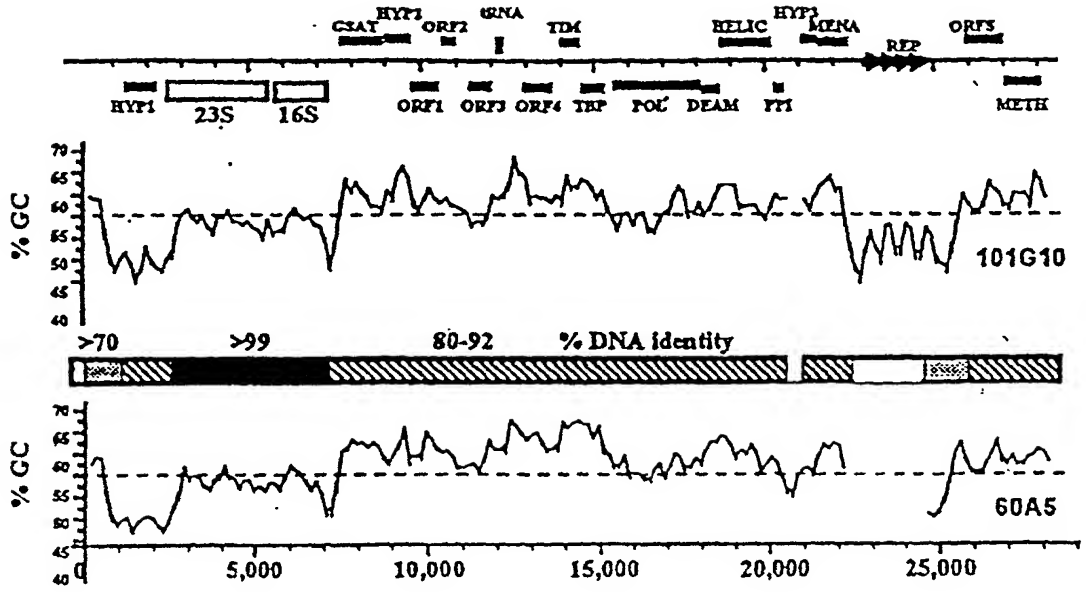
HYP1
CSAT
ORF2
tRNA
TDM
RELIC
HYP2
MRNA
REP
ORF5
HYP1
23S
16S
ORF1
ORF3
ORF4
TRP
POL
DEAM
PY1
METH
% GC
101G10
>70
>99
80-92
% DNA identity
% GC
60A5
5,000
10,000
15,000
20,000
25,000

Figure 2

SEQ. ID. NO.	Gene	Strain	TATA Box	Coding Start	TATA to Start (bp)
81	Hypoth 03	A	AAGCTAGACT TTTAAT TGGG ATCCGGCGGG GCGGCGCATG ---------- ----------		25
82		B	AAGCTAAACT TTTAAT TGGG ATCCGGCGAG CCGGCGCGTG ---------- ----------		
83	Hypoth 02	A	GGAAACTTTG ATTATA CGGG CGTGCTGCCC CGGGGCCCAT G--------- ----------		26
84		B	GGAAACTTTG ATTATA CGGG CGTACATTCC CGGGGCCCAT G--------- ----------		
85	ORF 02	A	AAGGCAAGGT AATAAT AGCC TGCCGTCTGT AACGGCCGTA TG-------- ----------		27
86		B	ACGGCAAGGT AATAAT AGCC TGCCGTCCGT ACCTGCCGTA TG-------- ----------		
87	ORF 03	A	CATGGAACTA GATATT AACC GGTTCCGCGG ATCCCATGCA TG-------- ----------		27
88		B	CATGGAACTA GATAAT AACC GGTCCCGCGG GTACAATGCA TG-------- ----------		
89	PPI	A	ATACCGAGAA GTTATA GCAG GGTATGGAAT GTGCGCGCGC ATG------- ----------		28
90		B	AGCACGACAA GTTATA GCAG GGTACAAAGG AGCAGCGCAC ATG------- ----------		
91	GSAT	A	ATCCGCCCTG ATTAAA TTAT GGGGGGAGCG GCCTGCTGCC GTG------- ----------		28
92		B	ATCCGGCCTC ATTAAA TTAC GGGGGGTACA ACCTGCTGCC GTG------- ----------		
93	ORF 05	A	CCTTCATACA CATAAA TCCC GCTTGGATGT GCGGCTGCGC ATG------- ----------		28
94		B	ACTTCATACA CATAAA TCCC GCCTGAACGG TCGTCCGCGC ATG------- ----------		
95	deaminase	A	.GGCATATAC CATAAT ATGC CGGGCGGTGG CACCATGGCC GTTG------ ----------		29
96		B	CCGCATATAC CATAAT ATGC CGGGCGGGGG CAGGCTGCCC .GTG------ ----------		
97	RNA helic	A	TGTACGAAAC CATAAA ACAA CAGGCCGCGT CAGGGCCGCG CGTG------ ----------		29
98		B	GGGTAGAAAC CATAAA ACAA CAGGCCGCGG CAGGGCG.CG CGTG------ ----------		
99	ORF 06	A	..ACACGCAG TATAAA CGGG GGCCCGGGCG GCGCGTATCA CATG------ ----------		29
100		B	ATACACGTGG TATAAA CAGA GG.CCGGACG GCGCGGACCA CATG------ ----------		
101	tRNA-tyr	A	GCGATAGTTA TTTAAA ACTA GGATGCCGAT CACGGATCGT CCCA------ ----------		29
102		B	GCGATAGTTA TTTAAA ACTA GGATGCCGGG CACCCGTCGT CCCA------ ----------		
103	TBP	A	CCGGGCCCCG GTTAAA ATAG CG.CACGGGC GGATCCTGAC CAATG----- ----------		30
104		B	CCGGGCCCCG GTTAAA ATAG AGTGCGGCCG GGCACCGGAT CAATG----- ----------		
105	TIM	A	GCGTCGATAG AATAAA TACG CGCAGGGGGC CCCGTGGCGC GATCGCCCGT G---------		36
106		B	GCGTCGATAG AATAAA TACG CGC.GGGGCC GCGGTGC... GATCGCCCGT G---------		
107	Hypoth 01	A	ATTTCAACTA CATAAA TGCC TAGTTACGCA GAAATAGCAA ACGACGTACT TCGACTAATG		45
108		B	ACTTCAACTA CATAAA TGCC TAGCTACGCA GAAATATCAA ACAAAGTACT TCGACTAATG		
109	ORF 01	A	ACGGCAGGCT ATTATT ACCT TGCCTTGCGT TGTA //..G CGGGGTGCGG CAGGGGATG		52
110		B	ACGGCAGGCT ATTATT ACCT TGCCGTGTG. TACA //..G AGGGGGCCTG CCGGGAGTG		
111	Methylase	A	CTACAACGAT TTTAAG TCGG CGCCGGGGCA GCCG.//..G ATGTGGGGCA GGCAACATG		104
112		B	CTACAAAGAT TTTAAG ACGG CGCGGGTGCC GCGG.//..T GGCACGGGGG CCTATCTTG		
113	16S RNA	A	TCGGCGATGG TTTATA TGCC CATGGACGGG CCGATCCGAT CGTACGTGAC GC.//..AAT		220
114		B	CCGGCGATGG TTTATA TGCC CATGGACAAG GCGATCCGAT CGTACGTGAC GC.//..AAT		
	Archaeal promoter consensus		YTTAWA		

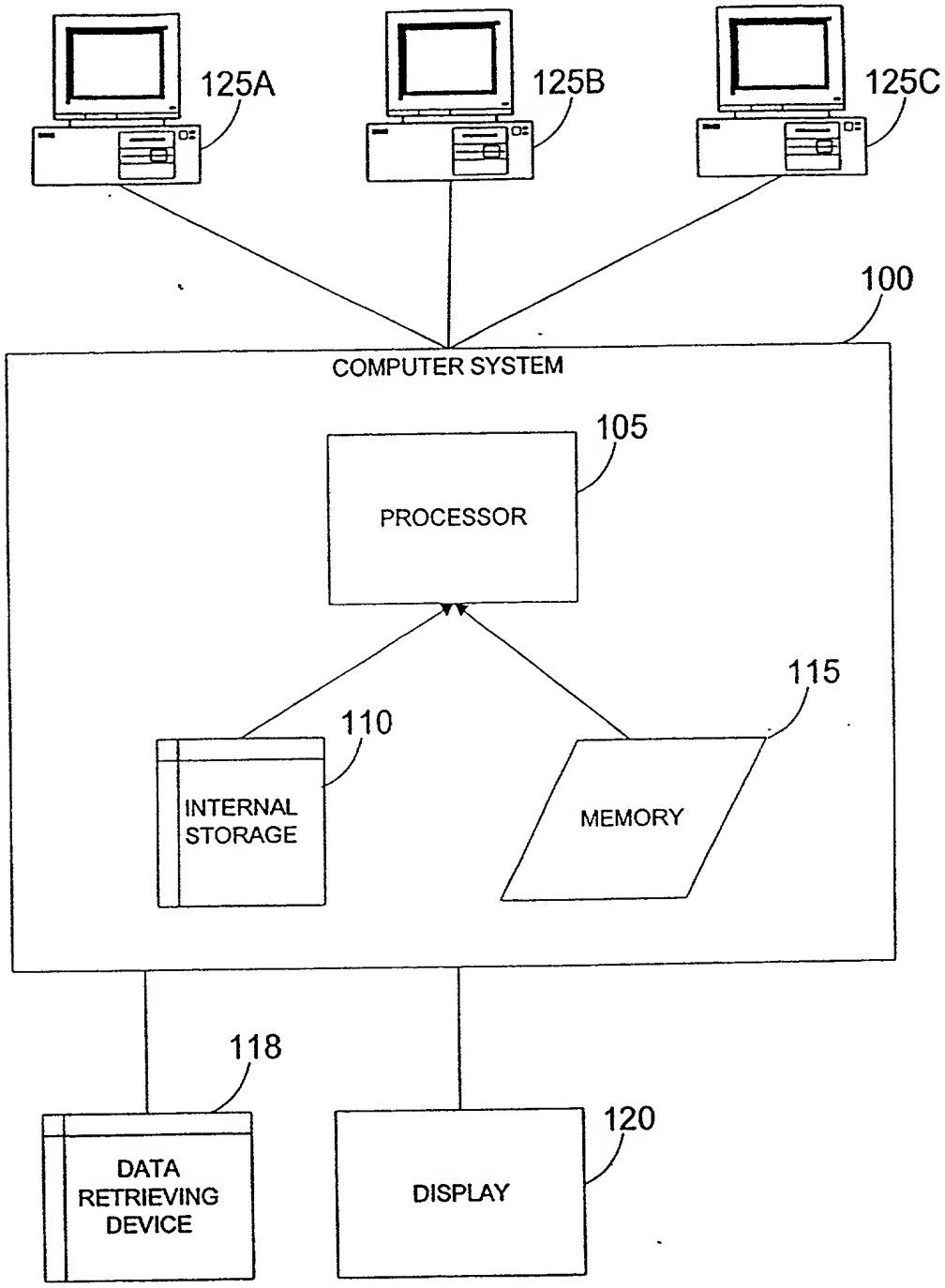
125A
125B
125C
100
COMPUTER SYSTEM
105
PROCESSOR
115
110
INTERNAL STORAGE
MEMORY
118
DATA RETRIEVING DEVICE
120
DISPLAY

FIGURE 3

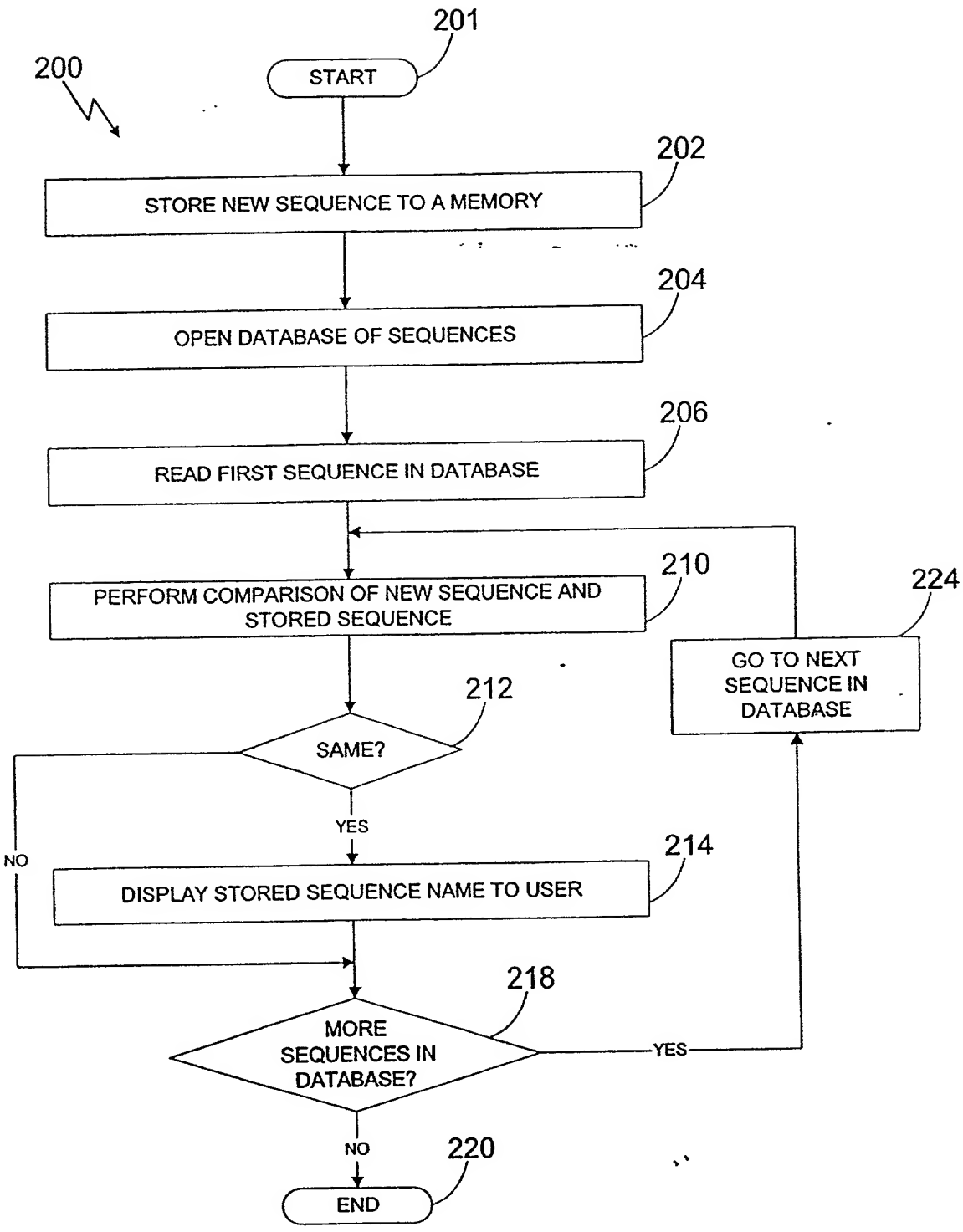
200
201
START
202
STORE NEW SEQUENCE TO A MEMORY
204
OPEN DATABASE OF SEQUENCES
206
READ FIRST SEQUENCE IN DATABASE
210
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
212
SAME?
YES
NO
214
DISPLAY STORED SEQUENCE NAME TO USER
218
MORE SEQUENCES IN DATABASE?
YES
NO
220
END
224
GO TO NEXT SEQUENCE IN DATABASE

FIGURE 4

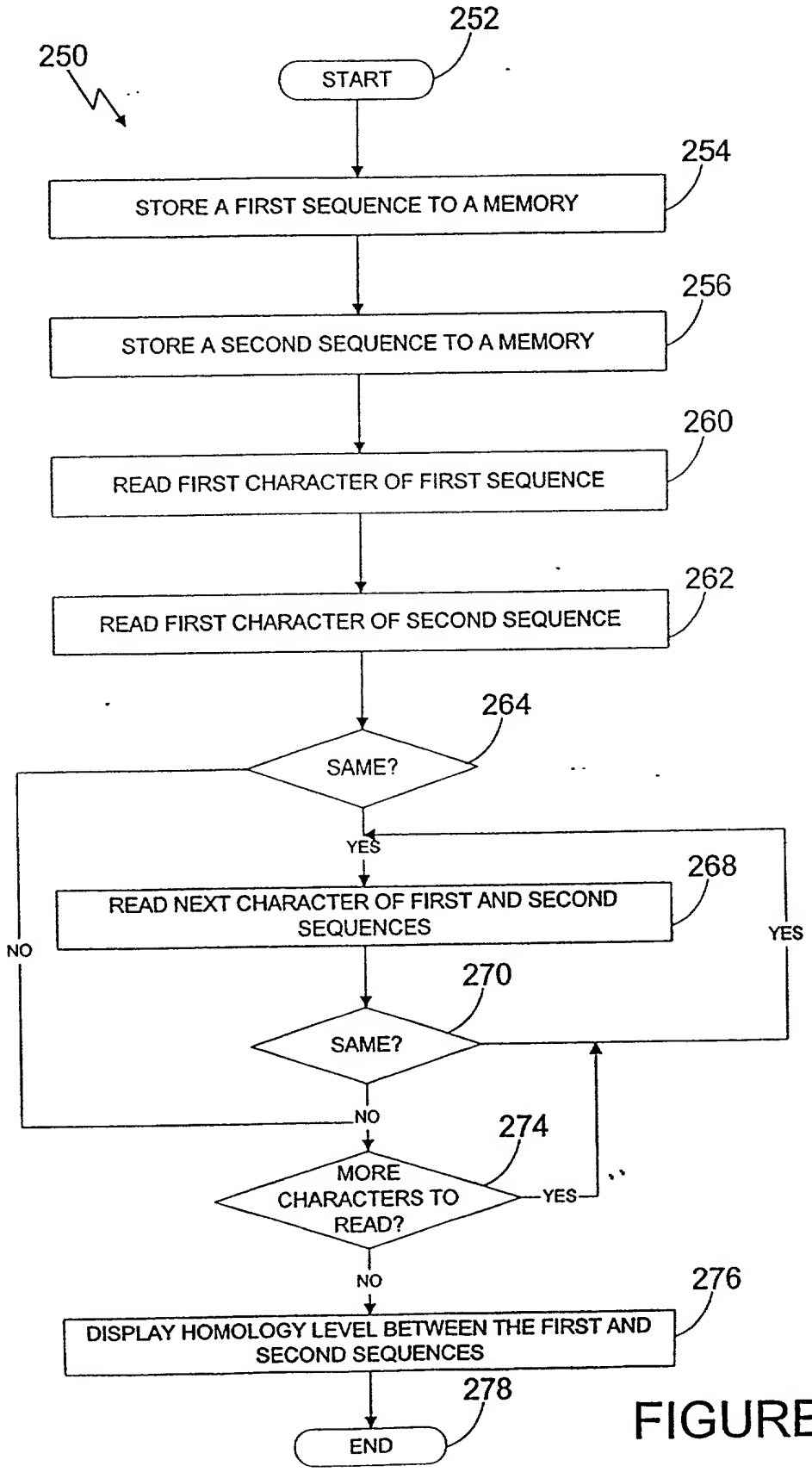
250
252
START
254
STORE A FIRST SEQUENCE TO A MEMORY
256
STORE A SECOND SEQUENCE TO A MEMORY
260
READ FIRST CHARACTER OF FIRST SEQUENCE
262
READ FIRST CHARACTER OF SECOND SEQUENCE
264
SAME?
YES
NO
268
READ NEXT CHARACTER OF FIRST AND SECOND SEQUENCES
YES
270
SAME?
NO
274
MORE CHARACTERS TO READ?
YES
NO
276
DISPLAY HOMOLOGY LEVEL BETWEEN THE FIRST AND SECOND SEQUENCES
278
END

FIGURE 5

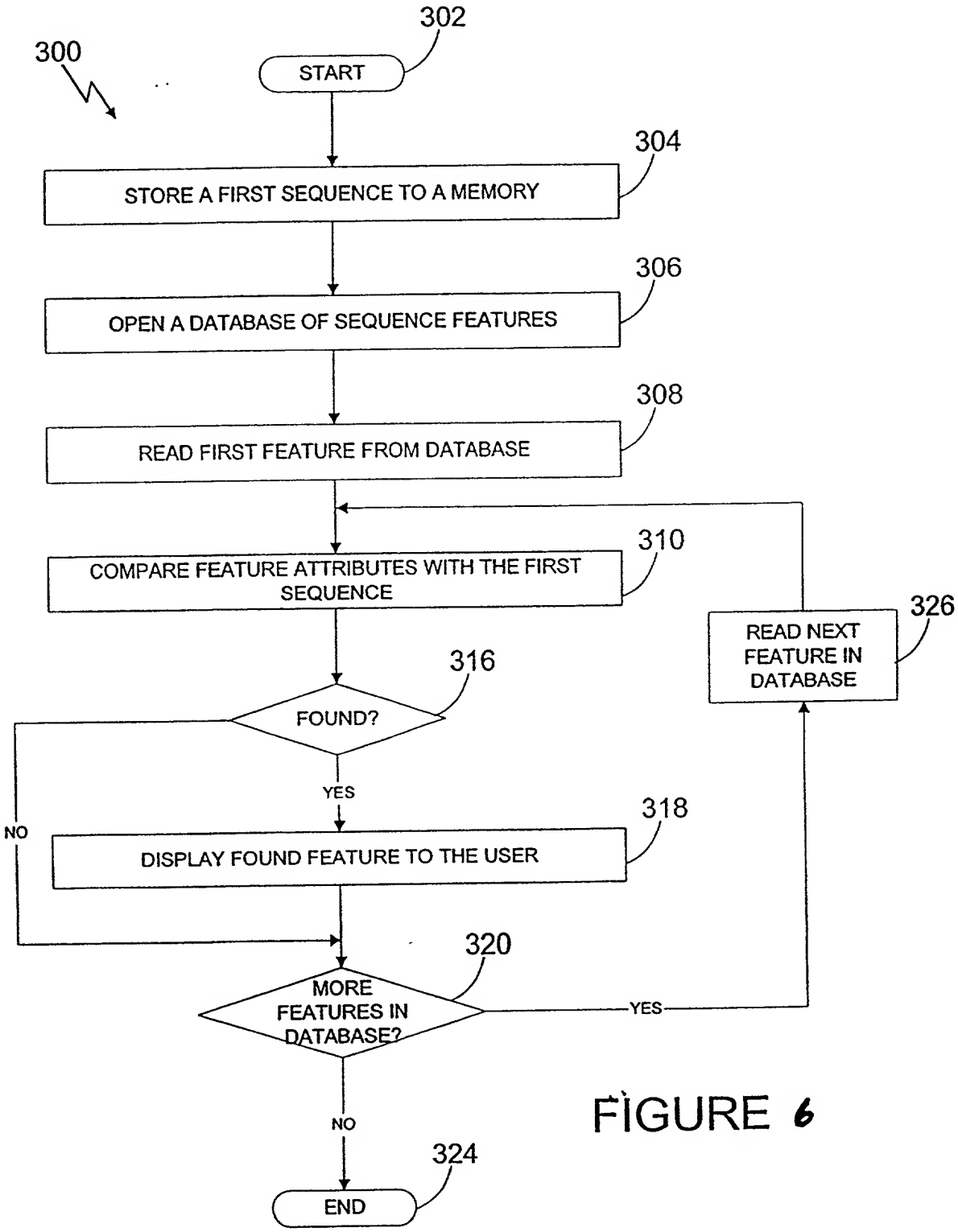
300
302
START
304
STORE A FIRST SEQUENCE TO A MEMORY
306
OPEN A DATABASE OF SEQUENCE FEATURES
308
READ FIRST FEATURE FROM DATABASE
310
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
316
FOUND?
YES
NO
318
DISPLAY FOUND FEATURE TO THE USER
320
MORE FEATURES IN DATABASE?
YES
NO
324
END
326
READ NEXT FEATURE IN DATABASE

FIGURE 6